

## SEQUENCE LISTING

<110> Smit, John

<120> CLEAVAGE OF CAULOBACTER PRODUCED  
RECOMBINANT FUSION PROTEINS

<130> 08106-004001

<140> 09/743,731

<141> 2001-01-12

<150> PCT/CA99/00637

<151> 1999-07-14

<150> CA 2,237,704

<151> 1998-07-14

<160> 11

<170> FastSEQ for Windows Version 4.0

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<212> PRT

<213> Artificial Sequence

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<223> Fusion protein

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<223> Synthetically generated peptide

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 Met Ala Tyr Thr Thr  
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gcc cag ttg gtg act gcg tac acc aac gcc aac ctc ggc aag gcg cct 163  
 Ala Gln Leu Val Thr Ala Tyr Thr Asn Ala Asn Leu Gly Lys Ala Pro  
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gac gcc gcc acc acg ctg acg ctc gac gcg tac gcg act caa acc cag 211  
 Asp Ala Ala Thr Thr Leu Thr Leu Asp Ala Tyr Ala Thr Gln Thr Gln  
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acg ggc ggc ctc tcg gac gcc gct gcg ctg acc aac acc ctg aag ctg 259  
 Thr Gly Gly Leu Ser Asp Ala Ala Ala Leu Thr Asn Thr Leu Lys Leu  
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gtc aac agc acg acg gct gtt gcc atc cag acc tac cag ttc ttc acc 307  
 Val Asn Ser Thr Thr Ala Val Ala Ile Gln Thr Tyr Gln Phe Phe Thr  
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ggc gtt gcc ccg tcg gcc gct ggt ctg gac ttc ctg gtc gac tcg acc 355  
 Gly Val Ala Pro Ser Ala Ala Gly Leu Asp Phe Leu Val Asp Ser Thr  
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Phe Thr Ala Ala Ala Asp Ile Asp Leu Ala Val Lys Ala Ala Leu Ile	
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ggc acc atc ctg aac gcc gcc acg gtg tcg ggc atc ggt ggt tac gcg	739
Gly Thr Ile Leu Asn Ala Ala Thr Val Ser Gly Ile Gly Gly Tyr Ala	
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Thr Ala Thr Ala Ala Met Ile Asn Asp Leu Ser Asp Gly Ala Leu Ser	
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Gly Val Ser Gly Ser Thr Leu Ser Leu Thr Thr Gly Thr Asp Thr Leu	
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Ala Ala Thr Leu Thr Val Gly Asp Thr Leu Ser Gly Gly Ala Gly Thr	
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Gly Val Thr Ile Ser Gly Ile Glu Thr Met Asn Val Thr Ser Gly Ala	
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Asn Thr Asn Thr Ser Gly Ala Ala Gln Thr Val Thr Ala Gly Ala Gly	
345 350 355	
cag aac ctg acc gcc acg acc gcc gct caa gcc gcg aac aac gtc gcc	1219
Gln Asn Leu Thr Ala Thr Thr Ala Ala Gln Ala Ala Asn Asn Val Ala	
360 365 370	
gtc gac ggg cgc gcc aac gtc acc gtc gcc tcg acg ggc gtg acc tcg	1267
Val Asp Gly Arg Ala Asn Val Thr Val Ala Ser Thr Gly Val Thr Ser	
375 380 385	
ggc acg acc acg gtc ggc gcc aac tcg gcc gct tcg ggc acc gtg tcg	1315

Gly Thr Thr Thr Val	Gly Ala Asn Ser Ala Ala	Ser Gly Thr Val Ser	
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Val Ser Val Ala Asn Ser Ser Thr Thr Thr Thr Gly Ala Ile Ala Val			
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Thr Gly Gly Thr Ala Val Thr Val Ala Gln Thr Ala Gly Asn Ala Val			
	425	430	435
aac acc acg ttg acg caa gcc gac gtg acc gtg acc ggt aac tcc agc			1459
Asn Thr Thr Leu Thr Gln Ala Asp Val Thr Val Thr Gly Asn Ser Ser			
	440	445	450
acc acg gcc gtg acg gtc acc caa acc gcc gcc gcc acc gcc ggc gct			1507
Thr Thr Ala Val Thr Val Thr Gln Thr Ala Ala Ala Thr Ala Gly Ala			
	455	460	465
acg gtc gcc ggt cgc gtc aac ggc gct gtg acg atc acc gac tct gcc			1555
Thr Val Ala Gly Arg Val Asn Gly Ala Val Thr Ile Thr Asp Ser Ala			
	470	475	480
gcc gcc tcg gcc acg acc gcc ggc aag atc gcc acg gtc acc ctg ggc			1603
Ala Ala Ser Ala Thr Thr Ala Gly Lys Ile Ala Thr Val Thr Leu Gly			
	490	495	500
agc ttc ggc gcc gcc acg atc gac tcg agc gct ctg acg acc gtc aac			1651
Ser Phe Gly Ala Ala Thr Ile Asp Ser Ser Ala Leu Thr Thr Val Asn			
	505	510	515
ctg tcg ggc acg ggc acc tcg ctc ggc atc ggc cgc ggc gct ctg acc			1699
Leu Ser Gly Thr Gly Thr Ser Leu Gly Ile Gly Arg Gly Ala Leu Thr			
	520	525	530
gcc acg ccg acc gcc aac acc ctg acc ctg aac gtc aat ggt ctg acg			1747
Ala Thr Pro Thr Ala Asn Thr Leu Thr Leu Asn Val Asn Gly Leu Thr			
	535	540	545
acg acc ggc gcg atc acg gac tcg gaa gcg gct gct gac gat ggt ttc			1795
Thr Thr Gly Ala Ile Thr Asp Ser Glu Ala Ala Ala Asp Asp Gly Phe			
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acc acc atc aac atc gct ggt tcg acc gcc tct tcg acg atc gcc agc			1843
Thr Thr Ile Asn Ile Ala Gly Ser Thr Ala Ser Ser Thr Ile Ala Ser			
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ctg gtg gcc gcc gac gcg acg acc ctg aac atc tcg ggc gac gct cgc			1891
Leu Val Ala Ala Asp Ala Thr Thr Leu Asn Ile Ser Gly Asp Ala Arg			
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gtc acg atc acc tcg cac acc gct gcc gcc ctg acg ggc atc acg gtg			1939
Val Thr Ile Thr Ser His Thr Ala Ala Ala Leu Thr Gly Ile Thr Val			
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Thr Asn Ser Val Gly Ala Thr Leu Gly Ala Glu Leu Ala Thr Gly Leu			

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acc aag gcg atc gtc atg ggc gcc ggc gac gac acc gtc acc gtc agc			2083
Thr Lys Ala Ile Val Met Gly Ala Gly Asp Asp Thr Val Thr Val Ser			
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tcg gcg acc ctg ggc gct ggt ggt tcg gtc aac ggc ggc gac ggc acc			2131
Ser Ala Thr Leu Gly Ala Gly Gly Ser Val Asn Gly Gly Asp Gly Thr			
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gac gtt ctg gtg gcc aac gtc aac ggt tcg tcg ttc agc gct gac ccg			2179
Asp Val Leu Val Ala Asn Val Asn Gly Ser Ser Phe Ser Ala Asp Pro			
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Ala Phe Gly Gly Phe Glu Thr Leu Arg Val Ala Gly Ala Ala Ala Gln			
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Gly Ser His Asn Ala Asn Gly Phe Thr Ala Leu Gln Leu Gly Ala Thr			
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gcg ggt gcg acg acc ttc acc aac gtt gcg gtg aat gtc ggc ctg acc			2323
Ala Gly Ala Thr Thr Phe Thr Asn Val Ala Val Asn Val Gly Leu Thr			
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gtt ctg gcg gct ccg acc ggt acg acg acc gtg acc ctg gcc aac gcc			2371
Val Leu Ala Ala Pro Thr Gly Thr Thr Thr Val Thr Leu Ala Asn Ala			
	745	750	755
acg ggc acc tcg gac gtg ttc aac ctg acc ctg tcg tcc tcg gcc gct			2419
Thr Gly Thr Ser Asp Val Phe Asn Leu Thr Leu Ser Ser Ser Ala Ala			
	760	765	770
ctg gcc gct ggt acg gtt gcg ctg gct ggc gtc gag acg gtg aac atc			2467
Leu Ala Ala Gly Thr Val Ala Leu Ala Gly Val Glu Thr Val Asn Ile			
	775	780	785
gcc gcc acc gac acc aac acg acc gct cac gtc gac acg ctg acg ctg			2515
Ala Ala Thr Asp Thr Asn Thr Thr Ala His Val Asp Thr Leu Thr Leu			
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caa gcc acc tcg gcc aag tcg atc gtg gtg acg ggc aac gcc ggt ctg			2563
Gln Ala Thr Ser Ala Lys Ser Ile Val Val Thr Gly Asn Ala Gly Leu			
	810	815	820
aac ctg acc aac acc ggc aac acg gct gtc acc agc ttc gac gcc agc			2611
Asn Leu Thr Asn Thr Gly Asn Thr Ala Val Thr Ser Phe Asp Ala Ser			
	825	830	835
gcc gtc acc ggc acg gct ccg gct gtg acc ttc gtg tcg gcc aac acc			2659
Ala Val Thr Gly Thr Ala Pro Ala Val Thr Phe Val Ser Ala Asn Thr			
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ctg acc ggt tcg gcc acc gcc aat gac acc atc atc ggt ggc gct ggc      2755
Leu Thr Gly Ser Ala Thr Ala Asn Asp Thr Ile Ile Gly Gly Ala Gly
870                      875                      880                      885

gct gac acc ctg gtc tac acc ggc ggt acg gac acc ttc acg ggt ggc      2803
Ala Asp Thr Leu Val Tyr Thr Gly Gly Thr Asp Thr Phe Thr Gly Gly
      890                      895                      900

acg ggc gcg gat atc ttc gat atc aac gct atc ggc acc tcg acc gct      2851
Thr Gly Ala Asp Ile Phe Asp Ile Asn Ala Ile Gly Thr Ser Thr Ala
      905                      910                      915

ttc gtg acg atc acc gac gcc gct gtc ggc gac aag ctc gac ctc gtc      2899
Phe Val Thr Ile Thr Asp Ala Ala Val Gly Asp Lys Leu Asp Leu Val
      920                      925                      930

ggc atc tcg acg aac ggc gct atc gct gac ggc gcc ttc ggc gct gcg      2947
Gly Ile Ser Thr Asn Gly Ala Ile Ala Asp Gly Ala Phe Gly Ala Ala
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gtc acc ctg ggc gct gct gcg acc ctg gct cag tac ctg gac gct gct      2995
Val Thr Leu Gly Ala Ala Ala Thr Leu Ala Gln Tyr Leu Asp Ala Ala
950                      955                      960                      965

gct gcc ggc gac ggc agc ggc acc tcg gtt gcc aag tgg ttc cag ttc      3043
Ala Ala Gly Asp Gly Ser Gly Thr Ser Val Ala Lys Trp Phe Gln Phe
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ggc ggc gac acc tat gtc gtc gtt gac agc tcg gct ggc gcg acc ttc      3091
Gly Gly Asp Thr Tyr Val Val Val Asp Ser Ser Ala Gly Ala Thr Phe
      985                      990                      995

gtc agc ggc gct gac gcg gtg atc aag ctg acc ggt ctg gtc acg ctg      3139
Val Ser Gly Ala Asp Ala Val Ile Lys Leu Thr Gly Leu Val Thr Leu
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acc acc tcg gcc ttc gcc acc gaa gtc ctg acg ctc gcc t aagcgaacgt      3189
Thr Thr Ser Ala Phe Ala Thr Glu Val Leu Thr Leu Ala
      1015                      1020                      1025

ctgatcctcg cctaggcgag gatcgctaga ctaagagacc ccgtctttccg aaagggaggc      3249
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<210> 5

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<212> PRT

<213> *Caulobacter crescentus*

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Tyr	Gln	Phe	Phe	Thr	Gly	Val	Ala	Pro	Ser	Ala	Ala	Gly	Leu	Asp	Phe
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Leu	Val	Asp	Ser	Thr	Thr	Asn	Thr	Asn	Asp	Leu	Asn	Asp	Ala	Tyr	Tyr
				85					90					95	
Ser	Lys	Phe	Ala	Gln	Glu	Asn	Arg	Phe	Ile	Asn	Phe	Ser	Ile	Asn	Leu
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Arg	Ala	Asn	Thr	Pro	Phe	Thr	Ala	Ala	Ala	Asp	Ile	Asp	Leu	Ala	Val
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Lys	Ala	Ala	Leu	Ile	Gly	Thr	Ile	Leu	Asn	Ala	Ala	Thr	Val	Ser	Gly
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Ala	Tyr	Pro	Ser	Ser	Gly	Val	Ser	Gly	Ser	Thr	Leu	Ser	Leu	Thr	Thr
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Gly	Thr	Asp	Thr	Leu	Thr	Gly	Thr	Ala	Asn	Asn	Asp	Thr	Phe	Val	Ala
			260					265					270		
Gly	Glu	Val	Ala	Gly	Ala	Ala	Thr	Leu	Thr	Val	Gly	Asp	Thr	Leu	Ser
		275					280					285			
Gly	Gly	Ala	Gly	Thr	Asp	Val	Leu	Asn	Trp	Val	Gln	Ala	Ala	Ala	Val
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Thr	Ala	Leu	Pro	Thr	Gly	Val	Thr	Ile	Ser	Gly	Ile	Glu	Thr	Met	Asn
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Gly	Leu	Thr	Ala	Leu	Asn	Thr	Asn	Thr	Ser	Gly	Ala	Ala	Gln	Thr	Val
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Ser	Gly	Thr	Val	Ser	Val	Ser	Val	Ala	Asn	Ser	Ser	Thr	Thr	Thr	Thr
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Gly	Ala	Ile	Ala	Val	Thr	Gly	Gly	Thr	Ala	Val	Thr	Val	Ala	Gln	Thr
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Ala	Gly	Asn	Ala	Val	Asn	Thr	Thr	Leu	Thr	Gln	Ala	Asp	Val	Thr	Val
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 Arg Gly Ala Leu Thr Ala Thr Pro Thr Ala Asn Thr Leu Thr Leu Asn  
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 545 550 555 560  
 Ala Asp Asp Gly Phe Thr Thr Ile Asn Ile Ala Gly Ser Thr Ala Ser  
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 645 650 655  
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 660 665 670  
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 675 680 685  
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 690 695 700  
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 740 745 750  
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 Asp Thr Leu Thr Leu Gln Ala Thr Ser Ala Lys Ser Ile Val Val Thr  
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 Gly Asn Ala Gly Leu Asn Leu Thr Asn Thr Gly Asn Thr Ala Val Thr  
 820 825 830  
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 Val Ser Ala Asn Thr Thr Val Gly Glu Val Val Thr Ile Arg Gly Gly  
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 Ala Gly Ala Asp Ser Leu Thr Gly Ser Ala Thr Ala Asn Asp Thr Ile  
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 Ile Gly Gly Ala Gly Ala Asp Thr Leu Val Tyr Thr Gly Gly Thr Asp  
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 Thr Phe Thr Gly Gly Thr Gly Ala Asp Ile Phe Asp Ile Asn Ala Ile  
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 Lys Leu Asp Leu Val Gly Ile Ser Thr Asn Gly Ala Ile Ala Asp Gly

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Ala Phe Gly Ala Ala Val Thr Leu Gly Ala Ala Ala Thr Leu Ala Gln
945              950              955              960
Tyr Leu Asp Ala Ala Ala Ala Gly Asp Gly Ser Gly Thr Ser Val Ala
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Lys Trp Phe Gln Phe Gly Gly Asp Thr Tyr Val Val Val Asp Ser Ser
      980              985              990
Ala Gly Ala Thr Phe Val Ser Gly Ala Asp Ala Val Ile Lys Leu Thr
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Gly Leu Val Thr Leu Thr Thr Ser Ala Phe Ala Thr Glu Val Leu Thr
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Leu Ala
1025

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<210> 6

<211> 306

<212> DNA

<213> Artificial Sequence

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<223> Synthetically generated polynucleotide

<221> CDS

<222> (1)...(306)

<400> 6

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tcg caa ggc gct ggc ctg ggt ggc cag ggc gct ggc gcg gcc gcg gcc      96
Ser Gln Gly Ala Gly Leu Gly Gly Gln Gly Ala Gly Ala Ala Ala Ala
      20              25              30

gct gcg gcc ggt ggc gct ggc cag ggc ggg ctg ggc tcg cag ggc gcc      144
Ala Ala Ala Gly Gly Ala Gly Gln Gly Gly Leu Gly Ser Gln Gly Ala
      35              40              45

ggc caa ggc gct ggc gcc gcg gcc gct gcg gcc ggt ggc gcc ggc cag      192
Gly Gln Gly Ala Gly Ala Ala Ala Ala Ala Gly Gly Ala Gly Gln
      50              55              60

ggt ggc tac ggc ggc ctg ggc agc cag ggc gcc ggt cgc ggc ggt cag      240
Gly Gly Tyr Gly Gly Leu Gly Ser Gln Gly Ala Gly Arg Gly Gly Gln
      65              70              75              80

ggc gcc ggt gcc gcg gcc gct gcg gcc ggt ggc gct ggg caa ggc ggc      288
Gly Ala Gly Ala Ala Ala Ala Ala Ala Ala Gly Gly Ala Gly Gln Gly Gly
      85              90              95

tac ggc ggt ctg gga tcc      306
Tyr Gly Gly Leu Gly Ser
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<210> 7

<211> 102

<212> PRT  
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<220>  
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 35 40 45  
 Gly Gln Gly Ala Gly Ala Ala Ala Ala Ala Gly Gly Ala Gly Gln  
 50 55 60  
 Gly Gly Tyr Gly Gly Leu Gly Ser Gln Gly Ala Gly Arg Gly Gly Gln  
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<210> 8  
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 <213> Infectious Pancreatic Necrosis Virus

<220>  
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 atg aac aca aac aag gca acc gca act tac ttg aaa tcc att atg ctt 48  
 Met Asn Thr Asn Lys Ala Thr Ala Thr Tyr Leu Lys Ser Ile Met Leu  
 1 5 10 15  
 cca gag act gga cca gca agc atc ccg gac gac ata acg gag aga cac 96  
 Pro Glu Thr Gly Pro Ala Ser Ile Pro Asp Asp Ile Thr Glu Arg His  
 20 25 30  
 atc tta aaa caa gag acc tcg tca tac aac tta gag gtc tcc gaa tca 144  
 Ile Leu Lys Gln Glu Thr Ser Ser Tyr Asn Leu Glu Val Ser Glu Ser  
 35 40 45  
 gga agt ggc att ctt gtt tgt ttc oct ggg gca cca ggc tca cgg atc 192  
 Gly Ser Gly Ile Leu Val Cys Phe Pro Gly Ala Pro Gly Ser Arg Ile  
 50 55 60  
 ggt gca cac tac aga tgg aat gcg aac cag acg ggg ctg gag ttc gac 240  
 Gly Ala His Tyr Arg Trp Asn Ala Asn Gln Thr Gly Leu Glu Phe Asp  
 65 70 75 80  
 cag tgg ctg gag acg tcg cag gac ctg aag aaa gcc ttc aac tac ggg 288  
 Gln Trp Leu Glu Thr Ser Gln Asp Leu Lys Lys Ala Phe Asn Tyr Gly  
 85 90 95  
 agg ctg atc tca agg aaa tac gac att caa agc tcc aca cta ccg gcc 336

Arg Leu Ile Ser Arg Lys Tyr Asp Ile Gln Ser Ser Thr Leu Pro Ala  
 100 105 110  
 ggt ctc tat gct ctg aac ggg acg ctc aac gct gcc acc ttc gaa ggc 384  
 Gly Leu Tyr Ala Leu Asn Gly Thr Leu Asn Ala Ala Thr Phe Glu Gly  
 115 120 125  
 agt ctg tct gag gtg gag agc ctg acc tac aat agc ctg atg tcc cta 432  
 Ser Leu Ser Glu Val Glu Ser Leu Thr Tyr Asn Ser Leu Met Ser Leu  
 130 135 140  
 act acg aac ccc cag gac aaa gcc aac aac cag ctg gtg acc aaa gga 480  
 Thr Thr Asn Pro Gln Asp Lys Ala Asn Asn Gln Leu Val Thr Lys Gly  
 145 150 155 160  
 gtc acc gtc ctg aat cta cca aca ggg ttc gac aaa cca tac gtc cgc 528  
 Val Thr Val Leu Asn Leu Pro Thr Gly Phe Asp Lys Pro Tyr Val Arg  
 165 170 175  
 cta gag gac gag aca ccc cag ggt ctc cag tca atg aac ggg gcc agg 576  
 Leu Glu Asp Glu Thr Pro Gln Gly Leu Gln Ser Met Asn Gly Ala Arg  
 180 185 190  
 ctg agg tgc aca gct gca att gca cca cgg agg tac gag atc gac ctc 624  
 Leu Arg Cys Thr Ala Ala Ile Ala Pro Arg Arg Tyr Glu Ile Asp Leu  
 195 200 205  
 cca tcc caa agc cta ccc ccc gtt cct gcg aca gga acc ctc acc act 672  
 Pro Ser Gln Ser Leu Pro Pro Val Pro Ala Thr Gly Thr Leu Thr Thr  
 210 215 220  
 ctc tac gag gga aac gcc gac atc gtc agc tcc aca aca gtg acg gga 720  
 Leu Tyr Glu Gly Asn Ala Asp Ile Val Ser Ser Thr Thr Val Thr Gly  
 225 230 235 240  
 gac ata aac ttc agt ctg gca gaa cga ccc gca aac gag acc agg ttc 768  
 Asp Ile Asn Phe Ser Leu Ala Glu Arg Pro Ala Asn Glu Thr Arg Phe  
 245 250 255  
 gac ttc cag ctg 780  
 Asp Phe Gln Leu  
 260

<210> 9  
 <211> 260  
 <212> PRT  
 <213> Infectious Pancreatic Necrosis Virus

<400> 9  
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 Pro Glu Thr Gly Pro Ala Ser Ile Pro Asp Asp Ile Thr Glu Arg His  
 20 25 30  
 Ile Leu Lys Gln Glu Thr Ser Ser Tyr Asn Leu Glu Val Ser Glu Ser  
 35 40 45  
 Gly Ser Gly Ile Leu Val Cys Phe Pro Gly Ala Pro Gly Ser Arg Ile

50                      55                      60  
 Gly Ala His Tyr Arg Trp Asn Ala Asn Gln Thr Gly Leu Glu Phe Asp  
 65                      70                      75                      80  
 Gln Trp Leu Glu Thr Ser Gln Asp Leu Lys Lys Ala Phe Asn Tyr Gly  
                     85                      90                      95  
 Arg Leu Ile Ser Arg Lys Tyr Asp Ile Gln Ser Ser Thr Leu Pro Ala  
                     100                      105                      110  
 Gly Leu Tyr Ala Leu Asn Gly Thr Leu Asn Ala Ala Thr Phe Glu Gly  
                     115                      120                      125  
 Ser Leu Ser Glu Val Glu Ser Leu Thr Tyr Asn Ser Leu Met Ser Leu  
                     130                      135                      140  
 Thr Thr Asn Pro Gln Asp Lys Ala Asn Asn Gln Leu Val Thr Lys Gly  
 145                      150                      155                      160  
 Val Thr Val Leu Asn Leu Pro Thr Gly Phe Asp Lys Pro Tyr Val Arg  
                     165                      170                      175  
 Leu Glu Asp Glu Thr Pro Gln Gly Leu Gln Ser Met Asn Gly Ala Arg  
                     180                      185                      190  
 Leu Arg Cys Thr Ala Ala Ile Ala Pro Arg Arg Tyr Glu Ile Asp Leu  
                     195                      200                      205  
 Pro Ser Gln Ser Leu Pro Pro Val Pro Ala Thr Gly Thr Leu Thr Thr  
                     210                      215                      220  
 Leu Tyr Glu Gly Asn Ala Asp Ile Val Ser Ser Thr Thr Val Thr Gly  
 225                      230                      235                      240  
 Asp Ile Asn Phe Ser Leu Ala Glu Arg Pro Ala Asn Glu Thr Arg Phe  
                     245                      250                      255  
 Asp Phe Gln Leu  
                     260

<210> 10  
 <211> 131  
 <212> PRT  
 <213> Escherichia coli

<400> 10  
 Phe Ala Cys Lys Thr Ala Asn Gly Thr Ala Ile Pro Ile Gly Gly Gly  
 1                      5                      10                      15  
 Ser Ala Asn Val Tyr Val Asn Leu Ala Pro Val Val Asn Val Gly Gln  
                     20                      25                      30  
 Asn Leu Val Val Asp Leu Ser Thr Gln Ile Phe Cys His Asn Asp Tyr  
                     35                      40                      45  
 Pro Glu Thr Ile Thr Asp Tyr Val Thr Leu Gln Arg Gly Ser Ala Ser  
 50                      55                      60  
 Tyr Pro Phe Pro Thr Thr Ser Glu Thr Pro Arg Val Val Tyr Asn Ser  
 65                      70                      75                      80  
 Arg Thr Asp Lys Pro Trp Pro Val Ala Leu Tyr Leu Thr Pro Val Ser  
                     85                      90                      95  
 Ser Ala Gly Gly Val Ala Ile Lys Ala Gly Ser Leu Ile Ala Val Leu  
                     100                      105                      110  
 Ile Leu Arg Gln Thr Asn Asn Tyr Asn Ser Asp Asp Phe Gln Cys Asp  
                     115                      120                      125  
 Val Ser Ala  
                     130

<210> 11  
 <211> 131  
 <212> PRT  
 <213> Escherichia coli

[illegible][illegible]